



CLC Main Workbench

Features & Benefits

Vice Chairman at the Department of Molecular Biology at University of Aarhus, Dr. Kim Kusk Mortensen:

CLC bio provides the newest algorithms and analyses available, which is fundamental for our research. We have chosen CLC Main Workbench because this single application can replace the whole range of outdated and expensive tools we have been using previously.

For Windows, Mac OS X, and Linux
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A comprehensive workbench for advanced DNA, RNA, & protein analyses

CLC Main Workbench includes all features and functions of CLC DNA Workbench, CLC RNA Workbench, and CLC Protein Workbench.

Advanced computer skills are not required. Due to a unique graphical user interface CLC Main Workbench is easy and intuitive to use, and the comprehensive user manual explains all the details. The full compatibility between all types of CLC workbenches provides strong support for efficient collaboration within research groups; allowing all researchers to easily share sequence data and research results.

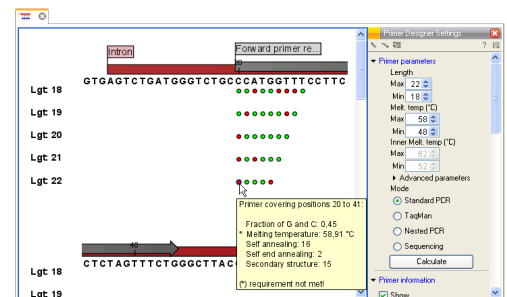
Assembly

CLC Main Workbench allows you to import, view, edit and analyze results from automated sequencing machines. Here, 3 sequencing reads have been automatically assembled into a contig sequence. The color intensity of each of the four nucleotides is shown as a trace graph under the called sequence of each sequencing read. The conflicts between the reads are marked with a red annotation.



Primer design

The primer design functionality in the workbench offers the user an unprecedented level of graphical interaction during the primer selection process. Primers can be designed for various experimental settings. In the primer editor the user can easily select regions to define primer sets and immediately view the properties of all primers using various levels of detail. When primer selection criteria, such as melting temperature and self-annealing values are adjusted, the effect can be immediately evaluated.



The integrated nature of the workbench makes it easy to design primers that span or cover a specific genetic element. Here the user has chosen to design primers that span a known genetic variation in an exon and requested that the primers must have a length between 18 and 22 nucleotides. Each available primer is indicated by a dot. Green dots indicate primers which fulfill all the selection criteria and red dots indicate primers which fail to meet one or more of the selection criteria.

Alignment

Contrary to most other alignment programs, CLC Main Workbench allows you to show the annotations of the individual sequences in a multiple sequence alignment. This can easily identify whether certain domains are conserved throughout an alignment.

Moreover, the information content of the alignment can be shown in form of a sequence logo, which can show information on highly conserved regions. The conservation of the individual residues in the alignments is shown as a histogram below the alignment.

Cloning

CLC Main Workbench offers graphically advanced in silico cloning and design of vectors for various purposes. Our approach to visual cloning is based on another philosophy than most other software tools, as the users are in total in control of the cloning process - contrary to the more or less automatic and noncontrollable cloning processes in other applications.

Adjustments of sequence overhangs by in silico nuclease treatment or filling in overhangs in both vector and insert are easily carried out and inspected visually.

BLAST/DB search

CLC Main Workbench offers to conduct BLAST searches on protein and DNA sequences or a combination of these using NCBI or it can run local if proprietary sequences are used. BLAST results are presented in a graphical overview together with a detailed tabular representation of the results. Sequence hits can easily be downloaded and analyzed further.

At the top is the alignment of all the hit sequences, and also displayed as annotations on the query sequence. At the bottom is a table showing all the hits which can be sorted and searched.

It is also possible to search your own data for homologous without the hassle of creating a BLAST database first. This can be done "on-the-fly" and can also be used to match primers against a larger sequence.

Plug-ins

CLC bio's modern and flexible IT architecture facilitates easy development of plug-ins for all of our bioinformatics workbenches, through our open API. When one or more plug-ins is installed on your computer, it is fully integrated with your CLC workbench - it runs as if it were one single (expanded) application.

You can develop your own plug-ins using our Developer Kit, or you can choose to use plug-ins developed by us or by third parties.

Available extensions

- Signal peptide prediction (SignalP)
- Transmembrane helix prediction (TMHMM)
- Sequence reader
- Extract annotations
- Recent items
- Bookmarks
- Vector NTI import

Available modules

- Additional alignments
- MLST

Contact your local sales representative or send an e-mail to sales@clcbio.com if you would like to try CLC Main Workbench.

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